SEQUENCE LISTING

<110> Barnett, Susan
      Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
      POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> PP01631.101

<140>
<141>

<150> 09/475,704
<151> 1999-12-30

<160> 45

<170> PatentIn Ver. 2.0

<210> 1
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 1
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<210> 2
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 2
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<210> 3
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      of HIV strain AF110965

<400> 3
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ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
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gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
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1

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<210> 4
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      of HIV strain AF110967

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caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
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gcccccggcc agatgcgcga ccccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac cccccccgtgc ccgtgggcga catctacaag 780
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tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
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2

<210> 5
<211> 141
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Env common
     region of HIV strain AF110968

<400> 5
accatcacca tcacctgccg catcaagcag atcatcaaca tgtggcagaa ggtgggccgc 60
gccatgtacg cccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
ctgctgaccc gcgacggcgg c   141

<210> 6
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
     gp120 coding region of HIV strain AF110968

<400> 6
agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
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ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
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aacagcacct acagccccag cttcaacggc accgagaaca gctgaacgg caccatcacc 1140
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gcccccccca tcgccggcaa cctgacctgc gagagcaaca tcaccggcct gctgctgacc 1260
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atgcgcgaca actggcgcaa cgagctgtac aagtacaagg tggtggagat caagcccctg 1380
ggcgtggccc ccaccgaggc caagcgccgc gtggtggagc gcgagaagcg c   1431

<210> 7
<211> 1944
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110968

<400> 7
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agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccc aggagatcgt gctggagaac 180
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atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgaccccct gtgcgtgacc 300
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gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcaccc aggcctgccc caaggtgagc 540
ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggcccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag cacccagctg ctgctgaacg gcagcctggc caagggcgag 720
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agcaaccgca gccacgacga gatctgggac aacatgacct ggatgcagtg ggaccgcgag 1800
atcaacaact acaccgacac catctaccgc ctgctggagg agagccagaa ccagcaggag 1860
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atcaccaact ggctgtggta catc 1944
```

<210> 8
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110968

<400> 8
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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgaccccct gtgcgtgacc 300
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4

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ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
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gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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<210> 9
<211> 2547
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence and gp160 coding region of HIV
      strain AF110968

<400> 9

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gagaccgagg tgcacaacgt gtgggccacc cacgcctgcg tgcccaccga ccccaacccc 240
caggagatcg tgctggagaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300
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aagaagagcg ccatcagcct gctggacacc atcgccatcg ccgtggccga gggcaccgac 2460
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<210> 10
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
      gp41 coding region of HIV strain AF110968

<400> 10
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gccgccagca tcaccctgac cgtgcaggcc cgcctgctgc tgagcggcat cgtgcagcag 120
cagaacaacc tgctgcgcgc catcgaggcc cagcagcacc tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcagac ccgcatcctg gccgtggagc gctacctgaa ggaccagcag 240
ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccgccgt gccctggaac 300
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6

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agcagctgga gcaaccgcag ccacgacgag atctgggaca acatgacctg gatgcagtgg 360
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cagcaggaga agaacgagaa ggacctgctg gccctggaca gctggcagaa cctgtggaac 480
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gccctgaagt acctgggcag cctggtgcag tactggggcc tggagctgaa gaagagcgcc 900
atcagcctgc tggacaccat cgccatcgcc gtggccgagg caccgaccg catcatcgag 960
ttcatccagc gcatctgccg cgccatccgc aacatccccc gccgcatccg ccagggcttc 1020
gaggccgccc tgcag                                                   1035

<210> 11
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Env
      common region of HIV strain AF110975

<400> 11
agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg cccgcgacgg cggc                                         144

<210> 12
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp120 coding region of HIV strain AF110975

<400> 12
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgccccccg ccggctacgc catcctgaag 600
tgcaagaaca caccagcaa cggcaccggc ccctgccaga cgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc ccccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca cgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccccca acaacaacac ccgcaagggc 840
atccgcatcg gcccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
```

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```
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg cccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg cccccagggc 1320
ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgc   1437
```

<210> 13
<211> 1950
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
        gp140 coding region of HIV strain AF110975

<400> 13
```
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaacccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga cgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gcccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg cccccccat cgagggcaac atcacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg cccccagggc 1320
ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440
gtgggcatcg gcgccgtgat cttcggcttc ctgggcgccg ccggcagcaa catgggcgcc 1500
gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
agcaacctgc tgcgcgccat cgaggcccag cagcacatgc tgcagctgac cgtgtggggc 1620
atcaagcagc tgcaggcccg cgtgctggcc atcgagcgct acctgaagga ccagcagctg 1680
ctgggcatct ggggctgcag cggcaagctg atctgcacca ccaccgtgcc ctggaacagc 1740
agctggagca acaagaccca gggcgagatc tgggagaaca tgacctggat gcagtgggac 1800
aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga acgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
ttcaacatca gcaactggct gtggtacatc                                 1950
```

<210> 14
```

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<211> 2493
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      gp160 coding region of HIV strain AF110975

<400> 14
agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcacccaggc ctgccccaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca caacaacac ccgcaagggc 840
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caggcccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
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aagctgttca acagcagcta caacggcacc agctaccgcg cgaccgagag caacagcagc 1140
atcatcaccc tgccctgccg catcaagcag atcatcgaca tgtggcagaa ggtgggccgc 1200
gccatctacg cccccccccat cgagggcaac atcaacctgca gcagcagcat caccggcctg 1260
ctgctggccc gcgacggcgg cctggacaac atcaccaccg agatcttccg ccccccagggc 1320
ggcgacatga aggacaactg cgcgaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggcccccac cgaggccaag cgccgcgtgg tggagcgcga gaagcgcgcc 1440
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gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
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aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga cgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
ttcaacatca gcaactggct gtggtacatc aagatcttca tcatgatcgt gggcggcctg 1980
atcggcctgc gcatcatctt cgccgtgctg agcatcgtga ccgcgtgcg ccagggctac 2040
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ctggccctgg cctgggacga cctgcgcagc ctgtgcctgt tcagctacca ccgcctgcgc 2220
gacctgatcc tggtgaccgc ccgcgtggtg gagctgctgg gccgcagcag ccccccgcggc 2280
ctgcagcgcg gctgggaggc cctgaagtac ctgggcagcc tggtgcagta ctggggcctg 2340
gagctgaaga gagcgccac cagcctgctg gacagcatcg ccatcgccgt ggccgagggc 2400
accgaccgca tcatcgaggt gatccagcgc atctaccgcg ccttctgcaa catcccccgc 2460
cgcgtgcgcc agggcttcga ggccgcccctg cag                            2493

<210> 15
<211> 2565

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence and gp160 coding region of HIV
      strain AF110975

<400> 15
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atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120
tggcgcgagg ccagcaccac cctgttctgc gccagcgacg ccaaggccta cgagaaggag 180
gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagatc 240
gagctggaca acgtgaccga gaacttcaac atgtggaaga acgacatggt ggaccagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cccgcgtgaa gctgacccccc 360
ctgtgcgtga ccctgaagtg caccaactac agcaccaact acagcaacac catgaacgcc 420
accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc 480
gagctgcgcg acaagaagca gcaggtgtac gccctgttct acaagctgga catcgtgccc 540
ctgaacagca cagcagcga gtaccgcctg atcaactgca acaccagcgc catcacccag 600
gcctgcccca aggtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660
gccatcctga gtgcaagaa caacaccagc aacggcaccg gcccctgcca gaacgtgagc 720
accgtgcagt gcacccacgg catcaagccc gtggtgagca ccccccctgct gctgaacggc 780
agcctggccg agggcggcga gatcatcatc cgcagcaaga acctgagcaa caacgcctac 840
accatcatcg tgcacctgaa cgacagcgtg gagatcgtgt gcacccgccc caacaacaac 900
acccgcaagg gcatccgcat cggccccggc cagaccttct acgccaccga gaacatcatc 960
ggcgacatcc gccaggccca ctgcaacatc agcgccggcg agtggaacaa ggccgtgcag 1020
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agcggcggcg acctggagat caccacccac agcttcaact gccgcggcga gttcttctac 1140
tgcaacacca gcaagctgtt caacagcagc tacaacggca ccagctaccg cggcaccgag 1200
agcaacagca gcatcatcac cctgccctgc cgcatcaagc agatcatcga catgtggcag 1260
aaggtgggcc gcgccatcta cgcccccccc atcgagggca acatcacctg cagcagcagc 1320
atcaccggcc tgctgctggc ccgcgacggc ggcctggaca acatcaccac cgagatcttc 1380
cgcccccagg gcggcgacat gaaggacaac tggcgcaacg agctgtacaa gtacaaggtg 1440
gtggagatca agcccctggg cgtggcccccc accgaggcca agcgccgcgt ggtggagcgc 1500
gagaagcgcg ccgtgggcat cggcgccgtg atcttcggct tcctgggcgc cgccggcagc 1560
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gtgcagcagc agagcaacct gctgcgcgcc atcgaggccc agcagcacat gctgcagctg 1680
accgtgtggg gcatcaagca gctgcaggcc cgcgtgctgg ccatcgagcg ctacctgaag 1740
gaccagcagc tgctgggcat ctggggctgc agcggcaagc tgatctgcac caccaccgtg 1800
ccctggaaca gcagctggag caacaagacc cagggcgaga tctgggagaa catgacctgg 1860
atgcagtggg acaaggagat cagcaactac accggcatca tctaccgcct gctggaggag 1920
agccagaacc agcaggagca gaacgagaag gacctgctgg ccctggacag ccgcaacaac 1980
ctgtggagct ggttcaacat cagcaactgg ctgtggtaca tcaagatctt catcatgatc 2040
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cgccagggct acagccccct gagcttccag accctgaccc ccaaccccccg cggcctggac 2160
cgcctgggcc gcatcgagga ggagggcggc gagcaggacc gcgaccgcag catccgcctg 2220
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caccgcctgc gcgacctgat cctggtgacc gccccgcgtgg tggagctgct gggccgcagc 2340
agccccgcg gcctgcagcg cggctgggag gccctgaagt acctgggcag cctggtgcag 2400
tactggggcc tggagctgaa gaagagcgcc accagcctgc tggacagcat cgccatcgcc 2460
gtggccgagg gcaccgaccg catcatcgag gtgatccagc gcatctaccg cgccttctgc 2520
aacatccccc gccgcgtgcg ccagggcttc gaggccgccc tgcag   2565
```

<210> 16

<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic a
      gp41 coding region of HIV strain AF110975

<400> 16
gccgtgggca tcggcgccgt gatcttcggc ttcctgggcg ccgccggcag caacatgggc 60
gccgccagca tcaccctgac cgcccaggcc cgccagctgc tgagcggcat cgtgcagcag 120
cagagcaacc tgctgcgcgc catcgaggcc cagcagcaca tgctgcagct gaccgtgtgg 180
ggcatcaagc agctgcaggc ccgcgtgctg gccatcgagc gctacctgaa ggaccagcag 240
ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccaccgt gccctggaac 300
agcagctgga gcaacaagac ccagggcgag atctgggaga acatgacctg gatgcagtgg 360
gacaaggaga tcagcaacta caccggcatc atctaccgcc tgctggagga gagccagaac 420
cagcaggagc agaacgagaa ggacctgctg gccctggaca gccgcaacaa cctgtggagc 480
tggttcaaca tcagcaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcggcc tgcgcatcat cttcgccgtg ctgagcatcg tgaaccgcgt gcgccagggc 600
tacagccccc tgagcttcca gaccctgacc cccaaccccc gcggcctgga ccgcctgggc 660
cgcatcgagg aggagggcgg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
ttcctggccc tggcctggga cgacctgcgc agcctgtgcc tgttcagcta ccaccgcctg 780
cgcgacctga tcctggtgac cgcccgcgtg gtggagctgc tgggccgcag cagcccccgc 840
ggcctgcagc gcggctggga ggccctgaag tacctgggca gcctggtgca gtactggggc 900
ctggagctga agaagagcgc caccagcctg ctggacagca tcgccatcgc cgtggccgag 960
ggcaccgacc gcatcatcga ggtgatccag cgcatctacc gcgccttctg caacatcccc 1020
cgccgcgtgc gccagggctt cgaggccgcc ctgcag 1056

<210> 17
<211> 492
<212> PRT
<213> Human immunodeficiency virus

<400> 17
Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
1               5                   10                  15

Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
                20                  25                  30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
            35                  40                  45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
        50                  55                  60

His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
65                  70                  75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
                85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
                100                 105                 110

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Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln
                115           120           125

Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala
        130           135           140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys
145           150           155           160

Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly
            165           170           175

Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His
            180           185           190

Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala
        195           200           205

Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly
        210           215           220

Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
225           230           235           240

Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val
            245           250           255

Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val
            260           265           270

Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys
        275           280           285

Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala
    290           295           300

Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu
305           310           315           320

Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly
            325           330           335

Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly
            340           345           350

Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala
        355           360           365

Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
    370           375           380

Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
385           390           395           400

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Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
                405                 410             415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420                 425             430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
        435                 440             445

Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
    450                 455             460

Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser
465                 470             475                 480

Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln
                485                 490
```

```
<210> 18
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence of HIV strain AF110968

<400> 18
atgcgcgtga tgggcatcct gaagaactac cagcagtggt ggatgtgggg catcctgggc  60
ttctggatgc tgatcatcag c                                             81

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      signal sequence of HIV strain AF110975

<400> 19
atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggt ggatctgggg catcctgggc  60
ttctggatct gc                                                       72

<210> 20
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      coding sequence of HIV strain AF110965
```

<400> 20

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atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tggtgtgggc cagccgcgag 120
ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
atccgccagc tgcaccccgc cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
accgtggcca ccctgtactg cgtgcacgag aagatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggtgat cgaggagaag 480
gccttcagcc ccgaggtgat ccccatgttc accgccctga gcgagggcgc cacccccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
gacaccatca cgaggaggc cgccgagtgg accgcgtgc accccgtgca cgccggcccc 660
atcgccccccg gccagatgcg cgagccccgc ggcagcgaca tcgccggcac caccagcacc 720
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aagcgctgga tcatcctggg cctgaacaag atcgtgcgca tgtacagccc cgtgagcatc 840
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accctgcgcg ccgagcagag cacccaggag gtgaagaact ggatgaccga caccctgctg 960
gtgcagaacg ccaacccccga ctgcaagacc atcctgcgcg ccctgggccc cggcgccagc 1020
ctggaggaga tgatgaccgc ctgccagggc gtgggcggcc ccagccacaa ggcccgcgtg 1080
ctggccgagg ccatgagcca ggccaacacc agcgtgatga tgcagaagag caacttcaag 1140
ggcccccgcc gcatcgtgaa gtgcttcaac tgcggcaagg agggccacat cgcccgcaac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca aagggccgc 1320
cccggcaact tcctgcagag ccgccccgag cccaccgccc ccccccgccga gagcttccgc 1380
ttcgaggaga ccacccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgacccccctg agccagtaa                      1479
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<210> 21
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
      coding sequence of HIV strain AF110967

<400> 21

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atgggcgccc gcgccagcat cctgcgcggc gagaagctgg acaagtggga gaagatccgc 60
ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tggtgtgggc cagccgcgag 120
ctggagggct cgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
atgaagcagc tgcagcccgc cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
accgtggcca ccctgtactg cgtgcacgcc ggcatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag agccagcaga gacccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac ccccaggac 540
ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
gcccccggcc agatgcgcga ccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac ccccccgtgc ccgtgggcga catctacaag 780
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ctgcgcgccg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
cagaacgcca accccgactg caagaccatc ctgcgcgccc tgggcccccgg cgccaccctg 1020
```

```
gaggagatga tgaccgcctg ccagggcgtg ggcggccccg gccacaaggc ccgcgtgctg 1080
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tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
cccggcaact tcctgcagaa ccgcagcgag cccgccgccc ccaccgtgcc caccgccccc 1380
cccgccgaga gcttccgctt cgaggagacc accccgccc ccaagcagga gcccaaggac 1440
cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggcccccctg 1500
agccagtaa                                                        1509
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<210> 22
<211> 502
<212> PRT
<213> Human immunodeficiency virus

<400> 22

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Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1               5                  10                  15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
                20                  25      ·           30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
            35                  40                  45

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
        50                  55                  60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn
65                  70                  75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp
                85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
    ·           100                 105                 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
        115                 120                 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
    130                 135                 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
145                 150                 155                 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
                165                 170                 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
            180                 185                 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
        195                 200                 205
```

15

```
Trp Asp Arg Leu His Pro Val Gln Ala Gly Pro Val Ala Pro Gly Gln
210             215             220

Met Arg Asp Pro Arg Gly Ser Asp Ile Ala Gly Ala Thr Ser Thr Leu
225             230             235             240

Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Val Pro Val Gly
                245             250             255

Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
            260             265             270

Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
            275             280             285

Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
        290             295             300

Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
305             310             315             320

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
                325             330             335

Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
            340             345             350

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn
            355             360             365

Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
    370             375             380

Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
385             390             395             400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
            405             410             415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420             425             430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
        435             440             445

Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
    450             455             460

Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
465             470             475             480

Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
            485             490             495
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16

Ser Gly Pro Leu Ser Gln
         500

<210> 23
<211> 849
<212> PRT
<213> Human immunodeficiency virus

<400> 23
Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
 1   5   10   15

Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
                20   25   30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
            35   40   45

Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
         50   55   60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65   70   75   80

Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
                85   90   95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
            100   105   110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
        115   120   125

Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp
        130   135   140

Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr
145   150   155   160

Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu
                165   170   175

Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile
            180   185   190

Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
        195   200   205

Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu
    210   215   220

Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val
225   230   235   240

17

Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln
            245   250   255

Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser
            260   265   270

Glu Asn Leu Ala Asn Asn Ala Lys Ile Ile Ile Val Gln Leu Asn Lys
            275   280   285

Pro Val Lys Ile Val Cys Val Arg Pro Asn Asn Asn Thr Arg Lys Ser
    290   295   300

Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile
305   310   315   320

Gly Asp Ile Arg Gln Ala Tyr Cys Ile Ile Asn Lys Thr Glu Trp Asn
            325   330   335

Ser Thr Leu Gln Gly Val Ser Lys Lys Leu Glu Glu His Phe Ser Lys
            340   345   350

Lys Ala Ile Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
            355   360   365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Ser
    370   375   380

Gln Leu Phe Asn Ser Thr Tyr Ser Pro Ser Phe Asn Gly Thr Glu Asn
385   390   395   400

Lys Leu Asn Gly Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile
            405   410   415

Asn Met Trp Gln Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala
            420   425   430

Gly Asn Leu Thr Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
            435   440   445

Asp Gly Gly Lys Thr Gly Pro Asn Asp Thr Glu Ile Phe Arg Pro Gly
    450   455   460

Gly Gly Asp Met Arg Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys
465   470   475   480

Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg
            485   490   495

Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe
            500   505   510

Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile
            515   520   525

Thr Leu Thr Val Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln
    530   535   540

Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
545   550   555   560

Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Ile Leu Ala Val
                565   570   575

Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
            580   585   590

Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser
            595   600   605

Asn Arg Ser His Asp Glu Ile Trp Asp Asn Met Thr Trp Met Gln Trp
    610   615   620

Asp Arg Glu Ile Asn Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu
625   630   635   640

Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu
                645   650   655

Asp Ser Trp Gln Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu
            660   665   670

Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
            675   680   685

Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly
    690   695   700

Tyr Ser Pro Leu Pro Phe Gln Thr Leu Thr Pro Asn Pro Arg Glu Pro
705   710   715   720

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
            725   730   735

Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
            740   745   750

Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
            755   760   765

Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
    770   775   780

Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
785   790   795   800

Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
            805   810   815

19

Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
                820   825   830

Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
                835   840   845

Gln

<210> 24
<211> 855
<212> PRT
<213> Human immunodeficiency virus

<400> 24
Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
1   5   10   15

Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
                20   25   30

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
            35   40   45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
        50   55   60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
65   70   75   80

Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
                85   90   95

Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
            100   105   110

Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr
            115   120   125

Asn Tyr Ser Thr Asn Tyr Ser Asn Thr Met Asn Ala Thr Ser Tyr Asn
        130   135   140

Asn Asn Thr Thr Glu Glu Ile Lys Asn Cys Thr Phe Asn Met Thr Thr
145   150   155   160

Glu Leu Arg Asp Lys Lys Gln Gln Val Tyr Ala Leu Phe Tyr Lys Leu
                165   170   175

Asp Ile Val Pro Leu Asn Ser Asn Ser Ser Glu Tyr Arg Leu Ile Asn
            180   185   190

Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp
        195   200   205

20

```
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
    210             215             220

Cys Lys Asn Asn Thr Ser Asn Gly Thr Gly Pro Cys Gln Asn Val Ser
225             230             235             240

Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Pro Leu
            245             250             255

Leu Leu Asn Gly Ser Leu Ala Glu Gly Gly Glu Ile Ile Ile Arg Ser
            260             265             270

Lys Asn Leu Ser Asn Asn Ala Tyr Thr Ile Ile Val His Leu Asn Asp
            275             280             285

Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
    290             295             300

Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Glu Asn Ile Ile
305             310             315             320

Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Ala Gly Glu Trp Asn
            325             330             335

Lys Ala Val Gln Arg Val Ser Ala Lys Leu Arg Glu His Phe Pro Asn
            340             345             350

Lys Thr Ile Glu Phe Gln Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
            355             360             365

Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser
    370             375             380

Lys Leu Phe Asn Ser Ser Tyr Asn Gly Thr Ser Tyr Arg Gly Thr Glu
385             390             395             400

Ser Asn Ser Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
            405             410             415

Asp Met Trp Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu
            420             425             430

Gly Asn Ile Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg
            435             440             445

Asp Gly Gly Leu Asp Asn Ile Thr Thr Glu Ile Phe Arg Pro Gln Gly
    450             455             460

Gly Asp Met Lys Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys Val
465             470             475             480

Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg
            485             490             495
```

21

Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Ile Phe
            500   505   510

Gly Phe Leu Gly Ala Ala Gly Ser Asn Met Gly Ala Ala Ser Ile Thr
            515   520   525

Leu Thr Ala Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
            530   535   540

Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu
.545   550   555   560

Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Ile Glu
            565   570   575

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
            580   585   590

Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ser Ser Trp Ser Asn
            595   600   605

Lys Thr Gln Gly Glu Ile Trp Glu Asn Met Thr Trp Met Gln Trp Asp
    610   615   620

Lys Glu Ile Ser Asn Tyr Thr Gly Ile Ile Tyr Arg Leu Leu Glu Glu
625   630   635   640

Ser Gln Asn Gln Gln Glu Gln Asn Glu Lys Asp Leu Leu Ala Leu Asp
            645   650   655

Ser Arg Asn Asn Leu Trp Ser Trp Phe Asn Ile Ser Asn Trp Leu Trp
            660   665   670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
            675   680   685

Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr
    690   695   700

Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Asn Pro Arg Gly Leu Asp
705   710   715   720

Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg
            725   730   735

Ser Ile Arg Leu Val Gln Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu
            740   745   750

Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu
            755   760   765

Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly
    770   775   780

```
Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
785             790             795             800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
                805             810             815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
            820             825             830

Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
        835             840             845

Gly Phe Glu Ala Ala Leu Gln
    850             855


<210> 25
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 25
Asp Ile Lys Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1               5               10              15

Phe Phe Lys Thr
            20


<210> 26
<211> 60
<212> DNA
<213> Human immunodeficiency virus

<400> 26
gacataaaac aaggaccaaa agagcccttt agagactatg tagaccggtt ctttaaaacc 60

<210> 27
<211> 20
<212> PRT
<213> Human immunodeficiency virus

<400> 27
Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1               5               10              15

Phe Phe Lys Thr
            20


<210> 28
<211> 47
<212> PRT
<213> Human immunodeficiency virus
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<400> 28
Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
 1   5   10   15

Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
             20   25   30

Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
         35   40   45

<210> 29
<211> 48
<212> PRT
<213> Human immunodeficiency virus

<400> 29
Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
 1   5   10   15

Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
             20   25   30

Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
         35   40   45

<210> 30
<211> 2469
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PR975(+)

<400> 30
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cgcagcaact tcaagggccc caagcgcatc atcaagtgct tcaactgcgg caaggagggc 120
cacatcgccc gcaactgccg cgccccccgc aagaagggct gctggaagtg cggcaaggag 180
ggccaccaga tgaaggactg caccgagcgc caggccaact tcttccgcga ggacctggcc 240
ttcccccagg gcaaggcccg cgagttcccc agcgagcaga accgcgccaa cagccccacc 300
agccgcgagc tgcaggtgcg cggcgacaac ccccgcagcg aggccggcgc cgagcgccag 360
ggcaccctga acttccccca gatcacccctg tggcagcgcc ccctggtgag catcaaggtg 420
ggcggccaga tcaaggaggc cctgctggac accggcgccg acgacaccgt gctggaggag 480
atgagcctgc ccggcaagtg gaagcccaag atgatcggcg gcatcggcgg cttcatcaag 540
gtgcgccagt acgaccagat cctgatcgag atctgcggca agaaggccat cggcaccgtg 600
ctgatcggcc ccacccccgt gaacatcatc ggccgcaaca tgctgaccca gctgggctgc 660
accctgaact tccccatcag ccccatcgag accgtgcccg tgaagctgaa gcccggcatg 720
gacggcccca aggtgaagca gtggcccctg accgaggaga agatcaaggc cctgaccgcc 780
atctgcgagg agatggagaa ggagggcaag atcaccaaga tcggccccga gaacccctac 840
aacacccccg tgttcgccat caagaagaag gacagcacca agtggcgcaa gctggtggac 900
ttccgcgagc tgaacaagcg cacccaggac ttctgggagg tgcagctggg catcccccac 960
cccgccggcc tgaagaagaa gaagagcgtg accgtgctgg acgtgggcga cgcctacttc 1020
agcgtgcccc tggacgagga cttccgcaag tacaccgcct tcaccatccc cagcatcaac 1080

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aacgagaccc ccggcatccg ctaccagtac aacgtgctgc cccagggctg gaagggcagc 1140
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gagatcgtga tctaccagta catggacgac ctgtacgtgg gcagcgacct ggagatcggc 1260
cagcaccgcg ccaagatcga ggagctgcgc aagcacctgc tgcgctgggg cttcaccacc 1320
cccgacaaga agcaccagaa ggagcccccc ttcctgtgga tgggctacga gctgcacccc 1380
gacaagtgga ccgtgcagcc catcgagctg cccgagaagg agagctggac cgtgaacgac 1440
atccagaagc tggtgggcaa gctgaactgg gccagccaga tctaccccgg catcaaggtg 1500
cgccagctgt gcaagctgct gcgcggcgcc aaggccctga ccgacatcgt gcccctgacc 1560
gaggaggccg agctggagct ggccgagaac cgcgagatcc tgcgcgagcc cgtgcacggc 1620
gtgtactacg accccagcaa ggacctggtg gccgagatcc agaagcaggg ccacgaccag 1680
tggacctacc agatctacca ggagcccttc aagaacctga agaccggcaa gtacgccaag 1740
atgcgcaccg cccacaccaa cgacgtgaag cagctgaccg aggccgtgca gaagatcgcc 1800
atggagagca tcgtgatctg gggcaagacc cccaagttcc gcctgcccat ccagaaggag 1860
acctgggaga cctggtggac cgactactgg caggccacct ggatccccga gtgggagttc 1920
gtgaacaccc cccccctggt gaagctgtgg taccagctgg agaaggagcc catcatcggc 1980
gccgagacct tctacgtgga cggcgccgcc aaccgcgaga ccaagatcgg caaggccggc 2040
tacgtgaccg accggggccg gcagaagatc gtgagcctga ccgagaccac caaccagaag 2100
accgagctgc aggccatcca gctggccctg caggacagcg gcagcgaggt gaacatcgtg 2160
accgacagcc agtacgccct gggcatcatc caggcccagc ccgacaagag cgagagcgag 2220
ctggtgaacc agatcatcga gcagctgatc aagaaggaga aggtgtacct gagctgggtg 2280
cccgcccaca agggcatcgg cggcaacgag cagatcgaca agctggtgag caagggcatc 2340
cgcaaggtgc tgttcctgga cggcatcgat ggcggcatcg tgatctacca gtacatggac 2400
gacctgtacg tgggcagcgg cggccctagg atcgattaaa agcttcccgg ggctagcacc 2460
ggtgaattc                                                        2469
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<210> 31
<211> 2463
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PR975YM

<400> 31
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cgcagcaact tcaagggccc caagcgcatc atcaagtgct tcaactgcgg caaggagggc 120
cacatcgccc gcaactgccg cgccccccgc aagaagggct gctggaagtg cggcaaggag 180
ggccaccaga tgaaggactg caccgagcgc caggccaact tcttccgcga ggacctggcc 240
ttcccccagg gcaaggcccg cgagttcccc agcgagcaga ccgcgccaa cagccccacc 300
agccgcgagc tgcaggtgcg cggcgacaac ccccgcagcg aggccggcgc cgagcgccag 360
ggcaccctga acttccccca gatcaccctg tggcagcgcc ccctggtgag catcaaggtg 420
ggcggccaga tcaaggaggc cctgctggac accggcgccg acgacaccgt gctggaggag 480
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27

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28

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29

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